

```
<!--StartFragment-->RESULT 7
PCT-US02-22833-26
; Sequence 26, Application PC/TUS0222833
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti G.
; APPLICANT: HONNCHELL, Cynthia D.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: BARROSO, Ines
; APPLICANT: YUE, Henry
; APPLICANT: WARREN, Bridget A.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LEE, Ernestine A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: TRAN, Bao
; APPLICANT: LI, Joana X.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: ZEBARJADIAN, Yeganeh
; APPLICANT: TRAN, Uyen K.
; APPLICANT: YAO, Monique G.
; APPLICANT: PETERSON, David P.
; APPLICANT: LUO, Wen
; APPLICANT: LEHR-MASON, Patricia M.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1082 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/22833
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US 60/306,020
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/308,179
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/309,702
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/311,476
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,718
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,551
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/314,798
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/316,639
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/317,996
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 26
;   LENGTH: 3320
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
```

SEQ ID NO 1

PCT/US02/22833

Qy	1	ATGGCGCTCAGCTGACAAGAATGGCAGCAACCTCCCATCTGTGTCTGGTAGCCGCTGCAG	60
Db	282	ATGGCGCTCTGCTGACAAGAATGGCGGGAGCGTGTCTCTGTGTCCAGCAGCCGCTGCAG	341
Qy	61	AGCCGGAAGCCACCCAACCTCTCCATCACCATCCCGCCACC-----AGAGAGCCAGGCC	114
Db	342	AGCCGGAAGCCACCCAACCTCTCCATCACCATCCCGCCACCCGAGAAAGAGACCCAGGCC	401
Qy	115	CCCGGCGAGCAGGATAGCATGCTTCCTGAGAGGCGCAAGAACCCAGCCTACCTGAAGAGT	174
Db	402	CCTGGCGAGCAGGACAGCATGCTGCCTGAGAGG---AAGAACCCAGCCTACTTGAAGAGC	458
Qy	175	GTCAGCCTACAGGAGCCCCGGGGACGATGGCAGGAGGGCGCAGAGAAGCGCCCCGGCTTC	234
Db	459	GTCAGCCTCCAGGAGCCACGCAGCCGATGGCAGGAGAGTTAGAGAAGCGCCCTGGCTTC	518
Qy	235	CGCCGCCAGGCCTCCCTGTCCCAGAGCATCCGCAAGAGCACAGCCCAGTGGTTTGGGGTC	294
Db	519	CGCCGCCAGGCCTCACTGTCCCAGAGCATCCGCAAGGGCGCAGCCCAGTGGTTTGGAGTC	578
Qy	295	AGCGGCGACTGGGAGGGCAAGCGACAAAACCTGGCATCGTCGCAGCCTGCACCACTGCAGC	354
Db	579	AGCGGCGACTGGGAGGGGCAGCGGCAGCAGTGGCAGCGCCGCAGCCTGCACCACTGCAGC	638
Qy	355	GTGCACTATGGCCGCCTCAAGGCCTCGTGCCAGAGAGAACTGGAGCTGCCCAGCCAGGAG	414
Db	639	ATGCGCTACGGCCGCCTGAAGGCCTCGTGCCAGCGTGACCTGGAGCTCCCCAGCCAGGAG	698
Qy	415	GTGCCATCCTTCCAGGGCACTGAGTCTCCAAAACCGTGCAAGATGCCCAAGATTGTGGAT	474
Db	699	GCACCGTCTTCCAGGGCACTGAGTCCCCAAAGCCCTGCAAGATGCCCAAGATTGTGGAT	758
Qy	475	CCACTGGCTCGGGGTAGGGCCTTCCGCCATCCAGATGAGGTGGACCGGCCCTCACGCTGCC	534
Db	759	CCGCTGGCCCGGGGCCGGGCCTTCCGCCACCCGAGGAGATGGACAGGCCCCACGCCCTG	818
Qy	535	CACCCACCTCTGACTCCAGGGGTCTGTCTCTACATCCTTCACCAGTGTCCGCTCTGGC	594
Db	819	CACCCACCGTGACCCCCGGAGTCCTGTCCCTCACCTCCTTCACCAGTGTCCGTTCTGGC	878
Qy	595	TACTCCCATCTGCCCCGCCGCAAGAGGATATCTGTTGCCCATATGAGCTTTCAGGCAGCC	654
Db	879	TACTCCACCTGCCACGCCGCAAGAGAATGTCTGTGGCCACATGAGCTTGCAAGCTGCC	938
Qy	655	GCCGCCCTCCTCAAGGGGCGTTCCGTGCTAGATGCGACTGGGCAGCGGTGCCGGCATGTC	714
Db	939	GCTGCCCTCCTCAAGGGGCGCTCGGTGCTGGATGCCACCGACAGCGGTGCCGGGTGGTC	998
Qy	715	AAACGCAGCTTCGCTTACCCCAGCTTCCTGGAGGAGGATGCTGTGATGGAGCTGACACC	774
Db	999	AAGCGCAGCTTTGCCTTCCCGAGCTTCCTGGAGGAGGATGTGGTTCGATGGGGCAGACACG	1058
Qy	775	TTCGACTCCTCCTTTTTTTAGTAAGGAAGAAATGAGCTCCATGCCTGACGATGTCTTTGAG	834

Db	1059	TTTGACTCCTCCTTTTTTTAGTAAGGAAGAAATGAGCTCCATGCCTGATGATGCTCTTGAG	1118
Qy	835	TCCCCCCCCTCTCTGCCAGCTACTTCCGAGGTGTCACACTCTGCCTCCCCGGTCTCC	894
Db	1119	TCCCCCCCCTCTCTGCCAGCTACTTCCGAGGGATCCCACACTCAGCCTCCCTGTCTCC	1178
Qy	895	CCGGATGGAGTGACATCCCGCTAAAAGAATACAGCGGTGGCCGAGCCCTGGGTCCCCGGG	954
Db	1179	CCCGATGGGGTGCAAATCCCTCTGAAGGAGTA-----TGGCCGAGCCCCAGTCCCCGGG	1232
Qy	955	ACCCAGCGTGGCAAACGCATTGCCTCCAAAGTAAAGCACTTTGCATTTGACCGGAAGAAG	1014
Db	1233	CCCCGGCGCGGCAAGCGCATCGCCTCCAAGGTGAAGCACTTTGCCTTTGATCGGAAGAAG	1292
Qy	1015	AGGCACTACGGCTGGGTGTCGTGGGTAAGTGGCTCAACCGAAGCTATCGACGCAGCATC	1074
Db	1293	CGGCACTACGGCTCGGCGTGGTGGGCAACTGGCTGAACCGCAGCTACCGCCGCAGCATC	1352
Qy	1075	AGCAGCACCGTGACGCGGCAGCTGGAGAGCTTCGATAGCCACCGGCCCTACTTCACCTAC	1134
Db	1353	AGCAGCACTGTGACGCGGCAGCTGGAGAGCTTCGACAGCCACCGGCCCTACTTCACCTAC	1412
Qy	1135	TGGCTGACGTTTCGTTACATCATCATCACCTTGCTGGTGATCTGCACCTATGGCATCGCA	1194
Db	1413	TGGCTGACCTTCGTCCATGTATCATCATCACGCTGCTGGTGATTGTCACGTATGGCATCGCA	1472
Qy	1195	CCTGTGGGCTTTTGCCAGCACGTTACCACCCAGCTGGTGCTGAAGAACAGAGGCGTGAT	1254
Db	1473	CCCGTGGGCTTTTGCCAGCACGTCACCACCCAGCTGGTGCTGCGGAACAAAGGTGTGTAC	1532
Qy	1255	GAGAGCGTGAAGTACATCCAGCAGGAGAACTTCTGGATTGGCCCCAGCTCGATTGACCTC	1314
Db	1533	GAGAGCGTGAAGTACATCCAGCAGGAGAACTTCTGGGTTGGCCCCAGCTCGATTGACCTG	1592
Qy	1315	ATTCACCTGGGAGCAAAGTTCTCGCCCTGCATCCGGAAGGACCAGCAAATTGAGCAGCTG	1374
Db	1593	ATCCACCTGGGGGCCAAGTTCTCACCTGCATCCGGAAGGACGGGCAGATCGAGCAGCTG	1652
Qy	1375	GTACGGAGGGAGCGCGACATTGAGCGCACCTCTGGCTGCTGTGTCCAGAATGACCGCTCG	1434
Db	1653	GTGCTGCGCGAGCGAGACCTGGAGCGGGACTCAGGCTGCTGTGTCCAGAATGACCACTCC	1712
Qy	1435	GGCTGCATCCAGACCCTGAAGAAGGACTGCTCGGAGACTTTAGCCACGTTCTGTAAAGTGG	1494
Db	1713	GGATGCATCCAGACCCAGCGGAAGGACTGCTCGGAGACTTTGGCCACTTTTGTCAAGTGG	1772
Qy	1495	CAGAATGATACTGGGCCCTC---AGACAAGTCTGACCTGAGCCAGAAGCAGCCATCGGCG	1551
Db	1773	CAGGATGACACTGGGCCCCCATGGACAAGTCTGATCTGGGCCAGAAGCGGACTTCGGGG	1832
Qy	1552	GTTGTGTGCCACCAAGACCCCAGGACCTGTGAAGAGCCTGCCTCCAGTGGGGCCACATC	1611
Db	1833	GCTGTCTGCCACCAGGACCCCAGGACCTGCGAGGAGCCAGCCTCCAGCGGTGCCACATC	1892
Qy	1612	TGGCCTGATGACATTACCAAGTGGCCGATCTGCACAGAGCAGGCTCAGAGCAACCACACG	1671
Db	1893	TGGCCCGATGACATCACTAAGTGGCCGATCTGCACAGAGCAGGCCAGGAGCAACCACACA	1952
Qy	1672	GGCTTGTTGCACATAGACTGTAAGATCAAAGGCCGCCCTGCTGCATCGGCACCAAGGGC	1731
Db	1953	GGCTTCCTGCACATGGACTGCGAGATCAAAGGCCGCCCTGCTGCATCGGCACCAAGGGC	2012

Qy	1732	AGCTGCGAGATCACCACCTCCGAGTACTGTGAGTTTCATGCATGGCTATTTCCATGAAGAC	1791
Db	2013	AGCTGTGAGATCACCACCCGGGAATACTGTGAGTTCATGCACGGCTATTTCCATGAGGAA	2072
Qy	1792	GCGACGCTGTGTTCCAGGTGCACTGTTTAGACAAGGTGTGTGGGCTCCTGCCTTTCCTC	1851
Db	2073	GCAACACTCTGCTCCCAGGTGCACTGCTTGGACAAGGTGTGTGGGCTGCTGCCCTTCCTC	2132
Qy	1852	AACCCTGAGGTCCCTGACCAGTTCTACCGGATCTGGCTGTCTTTATTCTGCATGCTGGC	1911
Db	2133	AACCCTGAGGTCCCAGATCAGTTCTACAGGCTCTGGCTGTCTCTCTTCCTACATGCTGGC	2192
Qy	1912	ATAGTGCACCTGCCTTGTGTCTGTGGTCTTCCAAATGACCATCCTGAGGGACCTAGAGAAG	1971
Db	2193	GTGGTGCACCTGCCTCGTGTCTGTGGTCTTTCAAATGACCATCCTGAGGGACCTGGAGAAG	2252
Qy	1972	CTGGCCGGCTGGCACC GCATCTCCATCATCTTCATCCTTAGTGGCATTACAGGCAACCTG	2031
Db	2253	CTGGCCGGCTGGCACC GTATCGCCATCATCTTCATCCTCAGTGGCATCACAGGCAACCTC	2312
Qy	2032	GCCAGCGCCATCTTCCTCCCTACCGGGCAGAGGTGGGCCCAGCCGGGTGCGAGTTCGGC	2091
Db	2313	GCCAGTGCCATCTTTCTCCCATACCGGGCAGAGGTGGGCCCAGCCGGCTCACAGTTCGGC	2372
Qy	2092	CTCCTCGCCTGCCTCTTCGTGGAGCTGTTCCAGAGCTGGCAGCTGTTGGAGCGGCCGTGG	2151
Db	2373	CTCCTCGCCTGCCTCTTCGTGGAGCTCTTCAGAGCTGGCCGCTGCTGGAGAGGCCCTGG	2432
Qy	2152	AAGGCCTTCTTCAACCTGTGCGCCATTGTGCTTTTCCTCTTCATCTGTGGCCTCCTGCCC	2211
Db	2433	AAGGCCTTCTTCAACCTCTCGGCCATCGTGCTCTTCCTGTTTCATCTGTGGCCTCCTGCCC	2492
Qy	2212	TGGATAGACAACATCGCCACATCTTCGGGTTTCCTCAGCGGCATGCTTCTGGCCTTCGCC	2271
Db	2493	TGGATCGACAACATCGCCACATCTTCGGCTTCCTCAGTGGCCTGCTGCTGGCCTTCGCC	2552
Qy	2272	TTCCTGCCTTACATTACCTTCGGCACCAGCGACAAGTACCGCAAGCGAGCCCTCATCCTC	2331
Db	2553	TTCCTGCCCTACATCACCTTCGGCACCAGCGACAAGTACCGCAAGCGGGCACTCATCCTG	2612
Qy	2332	GTGTCGCTGCTGGTCTTTGCTGGGCTCTTTGCTTCCCTGGTGCTGTGGCTGTACATCTAC	2391
Db	2613	GTGTCACTGCTGGCCTTTGCCGGCCTCTTCGCCGCCCTCGTGCTGTGGCTGTACATCTAC	2672
Qy	2392	CCCATCAACTGGCCCTGGATCGAGTACCTCACCTGCTTTCCCTTCACCAGCCGCTTCTGT	2451
Db	2673	CCCATTAACCTGGCCCTGGATCGAGCACCTCACCTGCTTCCCTTCACCAGCCGCTTCTGC	2732
Qy	2452	GAGAAGTACGAGCTAGACCAGGTGCTACACTAA	2484
Db	2733	GAGAAGTATGAGCTGACCAGGTGCTGCACTGA	2765

```
<!--EndFragment-->
```

SEQ ID NO: 2

WO 2003027228-A2

&lt;!--StartFragment--&gt;RESULT 3

ADC42843

ID ADC42843 standard; protein; 827 AA.

XX

AC ADC42843;

XX

DT 18-DEC-2003 (first entry)

XX

DE REMAP protein #3.

XX

KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KW Antiallergic; Antidiabetic; REMAP; pathogenesis.

XX

OS Homo sapiens.

XX

PN WO2003027228-A2.

XX

PD 03-APR-2003.

XX

PF 16-JUL-2002; 2002WO-US022833.

XX

PR 17-JUL-2001; 2001US-0306020P.

PR 27-JUL-2001; 2001US-0308179P.

PR 02-AUG-2001; 2001US-0309702P.

PR 10-AUG-2001; 2001US-0311476P.

PR 10-AUG-2001; 2001US-0311551P.

PR 10-AUG-2001; 2001US-0311718P.

PR 24-AUG-2001; 2001US-0314798P.

PR 31-AUG-2001; 2001US-0316639P.

PR 07-SEP-2001; 2001US-0317996P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;

PI Lee EA, Baughn MR, Gorvad AE, Duggan BM, Tran B, Li JX;

PI Richardson TW, Elliott VS, Zebanjadian Y, Tran UK, Yao MG;

PI Peterson DP, Luo W, Lehr-Mason PM;

XX

DR WPI; 2003-421156/39.

XX

PT New human receptors and membrane-associated proteins (REMAP), useful for  
PT diagnosing, treating or preventing disorders associated with aberrant  
PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or  
PT stroke.

XX

PS Claim 1; SEQ ID NO 3; 115pp; English.

XX

CC The present invention relates to an isolated polypeptide. The  
CC polypeptides and polynucleotides are useful in diagnosing, treating and  
CC preventing disorders associated with aberrant expression of REMAP, such  
CC as cell proliferative, autoimmune/inflammatory, renal, neurological,  
CC cardiovascular, metabolic, developmental, endocrine, muscle,  
CC gastrointestinal, lipid metabolism or transport disorders, and viral  
CC infections. These are also useful in assessing the effects of exogenous  
CC compounds on the expression of nucleic acids and amino acid sequences of  
CC REMAP, in facilitating drug discovery process, and in investigating the  
CC pathogenesis of diseases or medical conditions. Expression and  
CC purification were achieved using bacterial or virus-based expression  
CC systems. The present sequence represents an REMAP protein of the  
CC invention.

SQ Sequence 827 AA;

Query Match 92.1%; Score 4088; DB 7; Length 827;  
Best Local Similarity 91.6%; Pred. No. 0;  
Matches 760; Conservative 31; Mismatches 33; Indels 6; Gaps 4;

Qy	1	MASADKNGSNLPSVSGSRLQSRKPPNLSITIPPP--ESQAPGEQDSMLPERRKNPAYLKS	58
Db	1	MASADKNGSGSVSSVSSSRLQSRKPPNLSITIPPEKETQAPGEQDSMLPE-RKNPAYLKS	59
Qy	59	VSLQEPRGRWQEGAEKRPGRFRRQASLSQSIRKSTAQWFGVSGDWEGKRQNWHRSLHHC	118
Db	60	VSLQEPRSRWQESSEKRPGRFRRQASLSQSIRKGAAQWFGVSGDWEGQRQWQRRSLHHC	119
Qy	119	VHYGRLKASCQRELELPSQEVPFSQGTESPKPKCKMPKIVDPLARGRAFRHPDEVDRPHAA	178
Db	120	MRYGRLKASCQRDLELPSQEAPFSQGTESPKPKCKMPKIVDPLARGRAFRHPPEEMDRPHAL	179
Qy	179	HPPLTPGVLSLTSTSVRSGYSHLPRRKRIsvAHMSFQAAAALLKGRSVLDATGQRCRHV	238
Db	180	HPPLTPGVLSLTSTSVRSGYSHLPRRKRMsvAHMSLQAAAALLKGRSVLDATGQRCRVV	239
Qy	239	KRSFAYPSFLEEDAVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGVPHSASPVS	298
Db	240	KRSFAFPSPFLEEDVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGIPHSASPVS	299
Qy	299	PDGVHIPLKEYSGGRALGPGTQRGKRIASKVKHFADFRRKRHYGLGVGNWLNRSYRRSI	358
Db	300	PDGVQIPLKEY--GRAPVPGPRRGKRIASKVKHFADFRRKRHYGLGVGNWLNRSYRRSI	357
Qy	359	SSTVQRQLESFDSHRPYFTYWLTFVHIIITLLVICTYGIAPVGFAQHVTTLVLKNRGVY	418
Db	358	SSTVQRQLESFDSHRPYFTYWLTFVHVIITLLVICTYGIAPVGFAQHVTTLVLNRKGVY	417
Qy	419	ESVKYIQQENFWIGPSSIDLHLGAKFSPCIRKDDQIEQLVRRERDIERTSGCCVQNDRS	478
Db	418	ESVKYIQQENFWVGPPSSIDLHLGAKFSPCIRKDGQIEQLVLRERDLERDSGCCVQNDHS	477
Qy	479	GCIQTLKKDCSETLATFVKWQNDTG-PSDKSDLSQKQPSAVVCHQDPRTCEEPASSGAHI	537
Db	478	GCIQTQRKDCSETLATFVKWQDDTGPPMDKSDLGQKRTSGAVCHQDPRTCEEPASSGAHI	537
Qy	538	WPDDITKWPICTEQAQSNHTGLLHIDCKIKGRPCCIGTKGSCEITTREYCEFMHGYFHED	597
Db	538	WPDDITKWPICTEQARSNHTGFLHMDCEIKGRPCCIGTKGSCEITTREYCEFMHGYFHEE	597
Qy	598	ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRIWLSLFLHAGIVHCLVSVVFQMTILRDLEK	657
Db	598	ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRLWLSLFLHAGVVHCLVSVVFQMTILRDLEK	657
Qy	658	LAGWHRISIIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLACLFVELFQSWQLLERPW	717
Db	658	LAGWHRIAIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLACLFVELFQSWPLLERPW	717
Qy	718	KAFFNLSAIVLFLFICGLLPWIDNIAHIFGFLSGMLLAFAPLPYITFGTSDKYRKRALIL	777
Db	718	KAFLNLSAIVLFLFICGLLPWIDNIAHIFGFLSGLLLAFAPLPYITFGTSDKYRKRALIL	777
Qy	778	VSLLVFAGLFASLVWLWLYIYPINWPWIEYLTCPFTSRFCEKYELDQVLH	827

Db 778 VSLLAFAGLFAALVLWLYIYPINWPWIEHLTCFPFTSRFCEKYELDQVLH 827

<!--EndFragment-->